Figure 1A

```
  1  CAAGCACTGTGCTAAAGTGTTTTTCATATGTCATGAAAAGTTGTGCCAGAAAATTATGGT   60

 61  TTGAACATGGGCAGTTTTCTCCTACCGTCAGCTATATCCACAAGCATCACATGAAGTGGA  120

121  GATCTGGCAGCTCTGTGTATTTCAGTCAAGTTCCACAATGAAACCTGACAATAATGGTAA  180

181  AAACCAATACGGACATCTGAGTAACTGGGGAATTGGCCTGCCTTGCATGTGAGCTTGATG  240

241  GAAGATTGGATATAGACGAGTTGATTATATTTTATGAAGTAGCAGCTCACTACCATCCAC  300

301  CATCCAGGGTTTAAACTACTTTTTCAGCATCACTTCACCTGTGGACTCTTATACATTTTG  360

361  ATTTCTTGGGGGAAAAATACTGGGATAAGAGGAGGTCATTTTTTAATAAGTTAGCATCCT  420

421  TTTCCCTTTCTTACAAGTTGATCCAAAGGATAAGGCTGTGACTCCATTGGATTGCACCTT  480

481  TAAATCAAAATAGCAGCAGCAGAAGAAAGGGACAATGGCTCTGAGTGGAAACTGTAGTCG  540
  1                                          M  A  L  S  G  N  C  S  R   9

541  TTATTATCCTCGAGAACAAGGGTCCGCAGTTCCCAACTCCTTCCCTGAGGTGGTAGAGCT  600
 10   Y  Y  Y  P  R  E  Q  G  S  A  V  P  N  S  F  P  E  V  V  E  L   29

601  GAATGTCGGGGGTCAAGTTTATTTTACTCGCCATTCCACATTGATAAGCATCCCTCATTC  660
 30   N  V  G  G  Q  V  Y  F  T  R  H  S  T  L  I  S  I  P  H  S   49

661  CCTCCTGTGGAAAATGTTTTCCCCAAAGAGAGACACGGCTAATGATCTAGCCAAGGACTC  720
 50   L  L  W  K  M  F  S  P  K  R  D  T  A  N  D  L  A  K  D  S   69

721  CAAGGGAAGGTTTTTCATTGACAGAGATGGATTCTTGTTCCGTTATATTCTGGACTATCT  780
 70   K  G  R  F  F  I  D  R  D  G  F  L  F  R  Y  I  L  D  Y  L   89

781  CAGGGACAGGCAGGTGGTCCTGCCTGATCACTTTCCAGAAAAAGGAAGACTGAAAAGGGA  840
 90   R  D  R  Q  V  V  L  P  D  H  F  P  E  K  G  R  L  K  R  E   109

841  AGCTGAATACTTCCAGCTCCCAGACTTGGTCAAACTCCTGACCCCCGATGAAATCAAGCA  900
110   A  E  Y  F  Q  L  P  D  L  V  K  L  L  T  P  D  E  I  K  Q   129

901  AAGCCCAGATGAATTCTGCCACAGTGACTTTGAAGATGCCTCCCAAGGAAGCGACACAAG  960
130   S  P  D  E  F  C  H  S  D  F  E  D  A  S  Q  G  S  D  T  R   149

961  AATCTGCCCCCCTTCCTCCCTGCTCCCTGCCGACCGCAAGTGGGGTTTCATTACTGTGGG  1020
150   I  C  P  P  S  S  L  L  P  A  D  R  K  W  G  F  I  T  V  G   169
```

Figure 1B

```
1021  TTACAGAGGATCCTGCACCTTGGGCAGAGAGGGACAGGCAGATGCCAAGTTTCGGAGAGT  1080
 170   Y  R  G  S  C  T  L  G  R  E  G  Q  A  D  A  K  F  R  R  V   189


1081  TCCCCGGATTTTGGTTTGTGGAAGGATTTCCTTGGCAAAAGAAGTCTTTGGAGAAACTTT  1140
 190   P  R  I  L  V  C  G  R  I  S  L  A  K  E  V  F  G  E  T  L   209


1141  GAATGAAAGCAGAGACCCTGATCGAGCCCCAGAAAGATACACCTCCAGATTTTATCTCAA  1200
 210   N  E  S  R  D  P  D  R  A  P  E  R  Y  T  S  R  F  Y  L  K   229


1201  ATTCAAGCACCTGGAAAGGGCTTTTGATATGTTGTCAGAGTGTGGATTCCACATGGTGGC  1260
 230   F  K  H  L  E  R  A  F  D  M  L  S  E  C̲  G̲  F̲  H̲  M̲  V̲  A̲   249


1261  CTGTAACTCATCGGTGACAGCATCTTTCATCAACCAATATACAGATGACAAGATCTGGTC  1320
 250   C̲  N̲  S̲  S̲  V̲  T̲  A̲  S̲  F̲  I̲  N̲  Q̲  Y̲  T̲  D  D  K  I  W  S   269


1321  AAGCTACACTGAATATGTCTTCTACCGTGAGCCTTCCAGATGGTCACCCTCACACTGCGA  1380
 270   S  Y  T  E  Y  V  F  Y  R  E  P  S  R  W  S  P  S  H  C  D   289


1381  TTGCTGCTGCAAGAATGGCAAAGGTGACAAAGAAGGGGAGAGCGGCACGTCTTGCAATGA  1440
 290   C  C  C  K  N  G  K  G  D  K  E  G  E  S  G  T  S  C  N  D   309


1441  CCTCTCCACATCTAGCTGCGACAGCCAGTCTGAGGCCAGCTCTCCCCAGGAGACGGTCAT  1500
 310   L  S  T  S  S  C  D  S  Q  S  E  A  S  S  P  Q  E  T  V  I   329


1501  CTGTGGTCCCGTGACACGCCAGACCAACATCCAGACTCTGGACCGTCCCATCAAGAAGGG  1560
 330   C  G  P  V  T  R  Q  T  N  I  Q  T  L  D  R  P  I  K  K  G   349


1561  CCCTGTCCAGCTGATCCAACAGTCAGAGATGCGGCGGAAAAGCGACTTACTCCGGATTCT  1620
 350   P  V  Q  L  I  Q  Q  S  E  M  R  R  K  S  D  L  L  R  I  L   369


1621  GACTTCAGGCTCCAGGGAATCGAACATGAGCAGCAAAAAAAAAGCTGTTAAAGAAAAGCT  1680
 370   T  S  G  S  R  E  S  N  M  S  S  K  K  K  A  V  K  E  K  L   389


1681  CTCAATTGAGGAGGAGCTGGAGAAATGTATCCAGGATTTCCTAAAAAAAAAAATTCCAGA  1740
 390   S  I  E  E  E  L  E  K  C  I  Q  D  F  L  K  K  K  I  P  D   409


1741  TCGGTTTCCTGAGAGAAAACATCCTTGGCAATCTGAACTTTTAAGGAAGTATCATCTATA  1800
 410   R  F  P  E  R  K  H  P  W  Q  S  E  L  L  R  K  Y  H  L     428


1801  AGGGAGGGCTGGGGCGGGGAAAAAAAAAAAAAAAGAGTCATTTTGAAATTAACCTCATAA  1860


1861  AAGGAATTCATATTTTAAAGGAAAAAAATACAACTAATGATGCACATTTCTTAGAACACA  1920


1921  ATAGTCCATTGATATACTACTGCCTACTTTACCTAGTTCACCTTAACATGTAAATCCACA  1980
```

Figure 1C

```
1981  GGGTAGATTTCTTTCTAGATGTGGAAGTACAAGAAAATCTTTTTTAGTTATTTGTTTGTT  2040

2041  TACTTCGTCCCATGTGCTAACTATCTTATATATAATGAGAGCCAGCTACGTAAAAGTAGC  2100

2101  TGAGAGGCCTTGGGAGTCATTTATCCCAAACTGGGTTTTTTCTCTCATCCTTCTACCTCC  2160

2161  CTCCTTTGAATGAGGGTATGGTAGAAAAAGATCTGGCCCAATGGCATAAGTTTGGAATTT  2220

2221  TTAATTTTGGTTTTTCCTTTTGTTTATGGGGTTGGGGGGAATGGCAGATTTATATGACTT  2280

2281  TTCACTCAAATCTATATGTGCCAGTTTATATTGACTCCGTATGCATGAGTATTTGTGCAA  2340

2341  CACAAGCACAACTAAGTATGTATATACACATGACGCACACGATGCCAGGGCCTAGACCTC  2400

2401  CCAAGGGCTGTGCTCCTGCTCCCAGCAGCCCTCTCTTAGAATATTTCAGATGGATGAGCT  2460

2461  TCTGACTCTTTCTTAAAATTCTTTTGGGAAGATTTCCCAGCCTTTCTTCACAACACTTTC  2520

2521  TAACATCAAATGACTCTCATCATCAACAAATTGTATTCCTTATTGTGAAATTAATACCCT  2580

2581  CAGGCTCCATTTTACTGCTTTGCTCTTTGTCTGCATTAAGAGAGGATGAGGAGAGCTGGT  2640

2641  CAAACATTCCTTGTGTTAAAAAAATCAAACATTCATATCCACAAAATTTTCTGCTAAATG  2700

2701  ACTCCACACTCAGCCTTCTCTACCCTGAACTGAATTATCACCCTTTTCTCCATGTTTTCA  2760

2761  GAGTTCTTACTGCCCACAGTTTAATGGTGTGGCCTTTCCACATAATCCACATTAAGTTCT  2820

2821  GTGTTCCTGTGTTGTTGTGGAACTAAGGACAACACACAGTACTTGAATAAGGGTCCGGCC  2880

2881  TTTTGTTTGTTTTAGAGAAAGTTGTATTCCACACACAACCTAATAATTTCTTATAAAAAT  2940

2941  TTTAAACTACAAAGCTACATTTTTACTTGCTTGTAGCCGTTTTTGTTTGCCTTTGGGATT  3000

3001  CGGGCTTTGGCTGTGCCCATGCTAGGATTTAGCTGTGTCATTTTTATGATGTCTGTAACA  3060

3061  ACCCAACAAGGTAACTGAAGCTCCAGAGTTAAGGTTTCAGATTTCTAAATGAAACTATCT  3120

3121  TTTTCAATTACATCCTGACTTGTATAGACACAGCCAAAAAGAAACTGTTAATAGCCATCC  3180
```

Figure 1D

```
3181  GTCCATGTAACTCTGTATTTTACTAAGGTACCAATAGCTCTTTCATAGACTTGTGCTACA  3240

3241  AGAAGGTTAAAAGACCAGTTTTATTTTCAGCATTCCTCATGCATTTCAGTGGTAACCAAA  3300

3301  AAATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTTATTGCGTGTG  3360

3361  TGTGCATGTGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATGATTAAAAAAAAAAA  3420

3421  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  3468
```

Figure 2A

```
1                                                    50
  K+betaM2   (1) -----MALSGNCSRYYPREQGSAVPNSEPEYVELNVGGQYYFTRHSTLIS
 AAF558201   (1) ------------------------MPEIIELNVGGVSYTTSLATMLQ
CAA20329.1   (1) ------------------------MTSVEDVITLNVGGTLYTTRSTLSK
    Y34129   (1) -----------------MDNGDWGYMNTEPVTLNVGGHLYTTSLATILR
    Y34125   (1) MSRPLITRSPASPLXNQGIPTPAQLTKSNAPVHLVGGHMYTSSLATILR

            51                                                   100
  K+betaM2  (46) IPESLLWKMFSP--KRDTANDEAKDSKGRFEIDRDGPLFRYILDYYRDRQ
 AAF558201  (24) DKSTLLAELFG-----EGRDSLAKDSKGRYEIDRDGPLFRYILDFLRDKA
CAA20329.1  (27) ETEPLLANLASGSLSEDEQANVVPLPDGTEGIDRDGPLFAYMLHFLRTDK
    Y34129  (33) YPPSVMLGAMFGG----D--FPTAHDPGGNYEIDRDGPLFRYMLNFLRTSE
    Y34125  (51) YPESRIGRLFDG----T-EPIVLLSLKQHYEIDRDGQMFRYILNFLRTSK

            101                                                  150
  K+betaM2  (94) WVLEHEPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS
 AAF558201  (69) LHLEEGENERQRLLREAHFKLTAMLECERSEKDAR-----------
CAA20329.1  (77) LSLEEQEREVARCKPEADEYRLERESTLLSNASSIS-PRPR---------
    Y34129  (77) LTLELDLKEFDLLREADEYQLEPLIQCLNDPKPLY-----------
    Y34125  (96) LLEPTDEKDYTLLYREACYFQLQPMLLEKERWKQDR-----------

            151                                                  200
  K+betaM2 (144) QGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGRSGQADAKFRKVPRIL
 AAF558201 (105) ------------PP-----GCITTGYRGSPQFGKDGLADVKFRKLSRIL
CAA20329.1 (117) -----TANGYNTITSSAETGGYITLGYRGTFAFGREGQADVKFRKLHRIL
    Y34129 (113) ------------PMDTFEEVVELSSTRELSKYSNPVAVTITQLIITTK
    Y34125 (132) -----------ETGRFSRPCECLVVRVAPDLGERITLSGEKSLIEEVL

            201                                                  250
  K+betaM2 (194) VCGRIELAKEVFGETLNESRDPDR-APERYLSRFYLKFKELERAFDMLSE
 AAF558201 (137) VCGRVAQCEEVFGETLNESRDPDHGGTDRYESRFFLKHCYIEQAFDNLHD
CAA20329.1 (162) VCGRATICREEVFABTLNESRDPGG--PGDGE-----------
    Y34129 (149) VHELEEGISSYFTKWNKHMMDTRD---CQVSPTFGPCDYHQEVSLHVHLM
    Y34125 (169) PEIGDVMCNSVNACWNHESTHVIR------FPLNGYCHLKSVQVLERLQQ

            251                                                  300
  K+betaM2 (243) CGEHMVACNSSVTASFIN-----QYTDDKIWSSYTEYVFYRSPSRWSPSH
 AAF558201 (187) HGVRMAGSCGSGTAGSAAEPKPGVDTEENRWNHYNEFVFIRE--------
CAA20329.1 (191) -----------------------------------------
    Y34129 (196) EYITKQGFTIRNTRVHHMSERANENTVEHNWTFCRLARKTDI--------
    Y34125 (213) RGPEIVGSCGGGVDSSQFSEYVLRRELARTPRVPSVIRIKQEPL------

            301                                                  350
  K+betaM2 (288) CDCCCKNGKGDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQT
 AAF558201 (229) -----------------------------------------
CAA20329.1 (191) -----------------------------------------
    Y34129 (238) -----------------------------------------
    Y34125 (257) -----------------------------------------

            351                                                  400
  K+betaM2 (338) NIQTLDRPIKKGPVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKE
 AAF558201 (229) -----------------------------------------
CAA20329.1 (191) -----------------------------------------
    Y34129 (238) -----------------------------------------
    Y34125 (257) -----------------------------------------
```
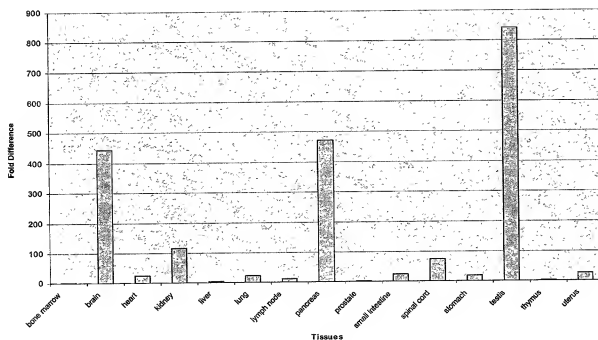
Figure 2B

```
                    401                                        441
   K+betaM2   (388) KLSIEEELEKCIQDFLKKKIPDRFPERKHPWQSELLRKYHL
  AAF558201   (229) ----------------------------------------
 CAA20329.1   (191) ----------------------------------------
    Y34129    (238) ----------------------------------------
    Y34125    (257) ----------------------------------------
  Consensus   (401)
```

Figure 3

Figure 4.

Protein	Genbank ID	Identities	Similarities
Human potassium channel K+Hnov28	gi|Y34129	31%	41%
Drosophila CG10830 protein	gi|AAF55820.1	52%	66%
Caenorhabditis K+ channel tetramerisation domain	gi|CAA20329.1	42%	51%
Human potassium channel K+Hnov27	gi|Y34125	32%	41%

Figure 5

K+betaM2 Relative Expression